

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 08:38:46 ; Search time 36 Seconds

(Without alignments)
143.088 Million cell updates/sec

Title: US-09-913-524-1

Perfect score: 143

Sequence: 1 PMSPSALRLQRPPEPAHANCHR 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671560 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_podent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	132	92.3	366	11 Q8VHP1	Q8VHP1 phodopus su
2	131	91.6	243	6 Q8SPR4	Q8SPR4 sus scrofa
3	97	67.8	329	13 Q98SC0	Q98SC0 meleagris g
4	66	46.2	352	13 Q98ED3	Q98ED3 oncorhynch
5	59	41.3	116	11 Q9DAI0	Q9DAI0 mus musculu
6	56	39.2	735	12 Q65567	Q65567 bovine herp
7	55.5	38.6	135	4 Q8WYGH	Q8WYGH homo sapien
8	55.5	38.8	368	4 Q8RAM0	Q8RAM0 homo sapien
9	55	38.5	435	5 Q9BL91	Q9BL91 canorhabdi
10	54.5	38.1	1832	2 Q9L8C8	Q9L8C8 polyanquim
11	54.5	38.1	1832	2 Q9K1Z8	Q9K1Z8 polyanquim
12	52	36.4	298	5 Q96676	Q96676 drosophila
13	52	36.4	2022	6 Q8WMP8	Q8WMP8 bos taurus
14	51.5	36.0	128	10 Q9LYX4	Q9LYX4 arabidopsis
15	51.5	36.0	159	10 Q8WID6	Q8WID6 arabidopsis
16	51	35.7	296	12 Q69118	Q69118 human herpe

17	50.5	35.3	135	11 Q9D7C0	Q9D7C0 mus muscula
18	50.5	35.3	135	11 Q9D6R7	Q9D6R7 mus muscula
19	50.5	35.3	135	11 Q9D6Q1	Q9D6Q1 mus muscula
20	50.5	35.3	2439	2 Q9L8C5	Q9L8C5 polyanquim
21	50.5	35.3	2439	2 Q9K1Z5	Q9K1Z5 polyanquim
22	50	35.0	155	4 Q96E55	Q96E55 homo sapien
23	50	35.0	365	16 Q9KDK7	Q9KDK7 bacillus ha
24	50	35.0	577	10 Q936B7	Q936B7 dancus caro
25	50	35.0	756	16 Q8XPY1	Q8XPY1 ralsstonia s
26	50	35.0	3122	12 P89459	P89459 herpes simp
27	49.5	34.6	656	4 Q96S18	Q96S18 homo sapien
28	49	34.3	303	2 Q54007	Q54007 salmoneila
29	49	34.3	316	16 Q93JM7	Q93JM7 ralsstonia s
30	49	34.3	469	4 Q92926	Q92926 homo sapien
31	49	34.3	1650	5 Q26816	Q26816 trypanosoma
32	49	34.3	2302	11 Q88488	Q88488 raltus norv
33	48.5	33.9	323	16 Q52485	Q52485 raltus norv
34	48	33.6	128	2 Q9XCD3	Q9XCD3 thermomonos
35	48	33.6	189	2 Q96RK1	Q96RK1 homo sapien
36	48	33.6	190	2 Q98175	Q98175 rhodobacter
37	48	33.6	320	4 Q98776	Q98776 homo sapien
38	48	33.6	332	11 Q991M7	Q991M7 mus muscula
39	48	33.6	398	4 Q969F8	Q969F8 homo sapien
40	48	33.6	535	6 Q95JM1	Q95JM1 macaca fasc
41	48	33.6	604	5 Q23838	Q23838 drosophila
42	48	33.6	828	11 Q9CX73	Q9CX73 mus musculu
43	48	33.6	1217	4 Q90UL5	Q90UL5 homo sapien
44	48	33.6	2024	2 Q9EWA3	Q9EWA3 streptomyce

ALIGNMENTS

RESULT 1
Q8VHP1 PRELIMINARY: PRT: 366 AA.

AC Q8VHP1: SEQUENCE FROM N.A.
RC TISSUE-OVARY:
RA Kenny H.A., Bernard D.J., Horton T.H., Woodruff T.K.;
RT "Photoperiod-dependent regulation of inhibin in Siberian Hamsters. I.
RT Ovarian Inhibin Production and Secretion.";
RL J. Endocrinol. 0:0-0(2002).
DR EMBL: AF432351; AAL67332.1; -;
DR InterPro: IPR002405; Inhibin_alpha.
DR InterPro: IPR001839; TGFb.
DR Pfam: PF00019; TGF_beta.1.
DR PRINTS: PR00669; INHIBINA.
DR PRODOM: PD000357; TGFb.1.
DR SMART: SM00204; TGFb.1.
DR PROSITE: PS00250; TGF_BETA_1; UNKNOWN_1.
KW SIGNAL.
FT SIGNAL. 1 233 POTENTIAL.
FT CHAIN. 234 366 INHIBIN ALPHA-SUBUNIT.
SQ SEQUENCE 366 AA: 39224 MW: F43DC2DB218B6256 CRC64;

Query Match 92.3%: Score 132; DB 11; Length 366;

Best Local Similarity 92.0%: Pred No. 9.6e-11;

Matches 23; Conservative 1; Mismatches 1; Gaps 0;

QY 1 PMSPSALRLQRPPEPAHANCHR 25
|||||

Db 241 FWSPAULRLQRPPEPAHANCGR 265

RESULT 2

Q8SPF4 PRELIMINARY: PRT: 243 AA.

AC Q8SPF4:

DT 01-JUN-2002 (TREMBlrel. 21, Created)

DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

DE Inhibin alpha subunit (Fragment).

GN INHA.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-95251210; PubMed=7733505;

RA Hiedler S., Jannaber U., Weimann C., Grandke R.;

RT "RFLP markers for the porcine INHA locus.";

RL Anim. Genet. 26:131-132(1995).

RN [2]

RP SEQUENCE FROM N.A.

RA Hiedler S., Keiner G., Geldermann H., Dzapo V.;

RT "Single nucleotide polymorphisms and PCR-RFLP linkage mapping of the

RT a-inhibin (INHA) gene, a QTL candidate for ovulation rate in swine.";

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY028465; AAK37741.1;

DR EMBL: AY028466; AAK37742.1;

FT NON_TER

FT NON_TER

FT NON_TER

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FT NON_TER

Query Match 67.8%; Score 97; DB 13; Length 329;

Best Local Similarity 68.0%; Pred. No. 7.4e-06;

Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 FWSPAULRLQRPPEPAHANCGR 25

DB 220 FWSPAULRLQRPPEPAHANCGR 244

RESULT 4

Q9DED3

AC Q9DED3: PRELIMINARY: PRT: 352 AA.

DT 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DE Inhibin.

GN INH.

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI_TaxID=8022;

RN [1]

RP SEQUENCE FROM N.A.

RA Tada T., Endo M., Hirono T., Takashima F., Aoki T.;

RT "Differential expression and cellular localization of activin and

RT inhibin mRNA in the rainbow trout ovary and testis.";

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AB044566; BAB19272.1;

DR EMBL: AB044567; BAB19273.1;

DR EMBL: AB044568; BAB19274.1;

DR EMBL: AB044569; BAB19275.1;

DR EMBL: AB044570; BAB19276.1;

DR EMBL: AB044571; BAB19277.1;

DR EMBL: AB044572; BAB19278.1;

DR EMBL: AB044573; BAB19279.1;

DR EMBL: AB044574; BAB19280.1;

DR EMBL: AB044575; BAB19281.1;

DR EMBL: AB044576; BAB19282.1;

DR EMBL: AB044577; BAB19283.1;

DR EMBL: AB044578; BAB19284.1;

DR EMBL: AB044579; BAB19285.1;

DR EMBL: AB044580; BAB19286.1;

DR EMBL: AB044581; BAB19287.1;

DR EMBL: AB044582; BAB19288.1;

DR EMBL: AB044583; BAB19289.1;

DR EMBL: AB044584; BAB19290.1;

DR EMBL: AB044585; BAB19291.1;

DR EMBL: AB044586; BAB19292.1;

DR EMBL: AB044587; BAB19293.1;

DR EMBL: AB044588; BAB19294.1;

DR EMBL: AB044589; BAB19295.1;

DR EMBL: AB044590; BAB19296.1;

DR EMBL: AB044591; BAB19297.1;

DR EMBL: AB044592; BAB19298.1;

DR EMBL: AB044593; BAB19299.1;

DR EMBL: AB044594; BAB19300.1;

DR EMBL: AB044595; BAB19301.1;

DR EMBL: AB044596; BAB19302.1;

DR EMBL: AB044597; BAB19303.1;

DR EMBL: AB044598; BAB19304.1;

Query Match 46.2%; Score 66; DB 13; Length 352;

Best Local Similarity 40.0%; Pred. No. 0.19;

Matches 10; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 FWSPAULRLQRPPEPAHANCGR 25

DB 243 FWSPAULRLQRPPEPAHANCGR 207

RESULT 5

Q9DAT0

AC Q9DAT0: PRELIMINARY: PRT: 116 AA.

DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DE Inhibin.

GN INH.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Scurionathii; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN=C57BL/6J; TISSUE=PLACENTA;

RT "Differential expression and cellular localization of activin and

RT inhibin mRNA in the rainbow trout ovary and testis.";

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AB044566; BAB19272.1;

DR EMBL: AB044567; BAB19273.1;

DR EMBL: AB044568; BAB19274.1;

DR EMBL: AB044569; BAB19275.1;

DR EMBL: AB044570; BAB19276.1;

DR EMBL: AB044571; BAB19277.1;

DR EMBL: AB044572; BAB19278.1;

DR EMBL: AB044573; BAB19279.1;

DR EMBL: AB044574; BAB19280.1;

DR EMBL: AB044575; BAB19281.1;

DR EMBL: AB044576; BAB19282.1;

DR EMBL: AB044577; BAB19283.1;

DR EMBL: AB044578; BAB19284.1;

DR EMBL: AB044579; BAB19285.1;

DR EMBL: AB044580; BAB19286.1;

DR EMBL: AB044581; BAB19287.1;

DR EMBL: AB044582; BAB19288.1;

DR EMBL: AB044583; BAB19289.1;

DR EMBL: AB044584; BAB19290.1;

DR EMBL: AB044585; BAB19291.1;

DR EMBL: AB044586; BAB19292.1;

DR EMBL: AB044587; BAB19293.1;

DR EMBL: AB044588; BAB19294.1;

DR EMBL: AB044589; BAB19295.1;

DR EMBL: AB044590; BAB19296.1;

DR EMBL: AB044591; BAB19297.1;

DR EMBL: AB044592; BAB19298.1;

DR EMBL: AB044593; BAB19299.1;

DR EMBL: AB044594; BAB19300.1;

DR EMBL: AB044595; BAB19301.1;

DR EMBL: AB044596; BAB19302.1;

DR EMBL: AB044597; BAB19303.1;

DR EMBL: AB044598; BAB19304.1;

DR EMBL: AB044599; BAB19305.1;

RA Fleischmann W., Gaasterland T., Gissi C., King H., Kochia H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Resole G., Quackenbush J.,
 RA Schriml L.M., Staudli F., Suzuki K., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boileau D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gastonclench S., Hill D., Hofmann M., Hume D.A., Kameya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberees P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,
 RA Wyszynski B., Yoshida K., Hasegawa Y., Kawai H., Kohlski S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.",
 RL Nature 409:685-690(2001).
 DR EMBL: AK005560; BAB24120.1; -;
 DR MBL: MGI:1917047; 160002914Rik.
 SQ SEQUENCE 116 AA: 13123 MW: 4633027654EMC20D CRC64:

Query Match 41.3%; Score 59; DB 11; Length 116;
 Best Local Similarity 71.4%; Pred. No. 0.6;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 12 RPEPPAHANCHR 25
 Db 99 RPEPPAHANCHR 112

RESULT 6
 Q65567 PRELIMINARY; PRT; 735 AA.

DT 01-NOV-1996 (TREMURel. 01, Created)
 DT 01-NOV-1996 (TREMURel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMURel. 17, Last annotation update)
 DE (COOPER) DNA (30 kb).
 CN UL15.
 OS Bovine herpesvirus 1.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicelloviruses.
 OX NCBI_TaxID=10320;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COOPER, AND JUHA;
 RX MEDLINE=9531343; PUBMED=7793062;
 RA Vitek C., Benes V., Lu Z., Kulish G.F., Paces V., Kock D.,
 RA Letchworth G.J., Schwyzer M.;
 RT "Nucleotide sequence analysis of a 30-kb region of the bovine
 herpesvirus 1 genome which exhibits a colinear gene arrangement with
 the UL21 to UL4 genes of herpes simplex virus.";
 RI Virology 210:100-108(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JUHA;
 RA Schwyzer M., Paces V., Letchworth G.J., Mista V., Rukh H.J.,
 RA Lowery D.E., Simard C., Bello L.J., Thiry E., Vitek C.,
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JUHA;
 RA Schwyzer M.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Z48053; CAAB8116.1; -;
 DR EMBL: A0004801; CA006117.1; -;
 DR InterPro: IPR003498; DNA_pack_C.
 DR InterPro: IPR003499; DNA_pack_N.
 DR Pfam: PF02459; DNA_pack_C.1.
 DR Pfam: PF02509; DNA_pack_N.1.
 SQ SEQUENCE 735 AA: 78902 MW: 0342935FA333801 CRC64:

Query Match 39.2%; Score 56; DB 12; Length 735;
 Best Local Similarity 55.0%; Pred. No. 9.9;
 Matches 11; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Oy 5 SALRLQRPPEPAHANCH 24
 Db 116 SALRFAPHPAFAHANCH 135

RESULT 7
 Q8WYG8 PRELIMINARY; PRT; 135 AA.
 ID Q8WYG8
 AC Q8WYG8;
 DT 01-MAR-2002 (TREMURel. 20, Created)
 DT 01-MAR-2002 (TREMURel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMURel. 20, Last annotation update)
 DE Hypothetical 15.1 kDa protein.
 GN PP2593.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gu J.R., Man D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
 RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Ji H.N., Yu Y.,
 RA Yu J., Han L.H.;
 RT "Novel human cDNA clones with function of inhibiting cancer cell
 growth.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF193049; AAC22477.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 135 AA: E8506635105F6A69 CRC64:

Query Match 48.8%; Score 55.5; DB 4; Length 135;
 Best Local Similarity 44.1%; Pred. No. 2.2;
 Matches 15; Conservative 3; Mismatches 5; Indels 11; Gaps 3;

Oy 1 PMSFALRLQRP-----EEV---AAVANCHR 25
 Db 6 PMAEA--RLQGPAPSHATQRLMTVAHQSHR 37

RESULT 8
 ID Q8TAM0 PRELIMINARY; PRT; 368 AA.
 AC Q8TAM0;
 DT 01-JUN-2002 (TREMURel. 21, Created)
 DT 01-JUN-2002 (TREMURel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMURel. 21, Last annotation update)
 DE G protein-coupled receptor 62.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RA Strausberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC026357; AAH26357.1; -;
 KW Receptor.
 SQ SEQUENCE 368 AA: 9050669D98012FBA CRC64:

Query Match 38.8%; Score 55.5; DB 4; Length 368;
 Best Local Similarity 66.7%; Pred. No. 5.9;
 Matches 12; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

Oy 2 WSPSA-LRLQRPPEPA 18
 Db 321 WFRALQQLQRPPECPA 338

RESULT 9
 Q9BL91 PRELIMINARY; PRT; 435 AA.

AC Q9H191;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, last annotation update)
 DE Hypothetical 48.6 kDa protein.
 GN Y18H1A.7.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Bonis C., Lamar B., Courtney L., Wohldmann P., Harrison M.;
 RT "The sequence of C. elegans cosmid Y18H1A.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Walerton R.;
 RT "Direct Submission.";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR FMBL; AC024751; AAK21510.2; -;
 KW Hypothetical protein.
 SQ SEQUENCE 435 AA; 48573 MW; 1DB7E011793AF18 CRC64;
 QY Query Match 38.5%; Score 55; DB 5; Length 435;
 Best Local Similarity 43.5%; Pred. No. 8.2;
 Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
 QY 3 SP5ALRLQRPPEPPAANACHR 25
 DB 384 SASAKTFKPPPEOPMCSNLRK 406
 QY18C8
 ID QY18C8 PRELIMINARY; PRT; 1832 AA.
 AC QY18C8;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)
 DE Polyketide synthase.
 GN EPOC.
 OS Polyangium cellulosum.
 OC Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
 OC Myxococcales; Sorangineae; Polyangiaceae; Polyangium.
 OX NCBI_TaxID=56;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SO CR90;
 RX MEDLINE=20130945; PubMed=10662695;
 RA Molnar T., Schupp T., Ono M., Zirkle R.E., Milnamow M.,
 RA Novak-Thompson B., Engel N., Toupet C., Stratmann A., Cyr D.D.,
 RA Grolach J., Mayo J.M., Hu A., Golf S., Schmid J., Ligon J.M.;
 RT "The biosynthetic gene cluster for the microtubule-stabilizing agents
 epothilones A and B from Sorangium cellulosum so ce90.";
 RL Chem. Biol. 7:97-109(2000).
 DR EMBL; AF210843; AAF26920.1; -;
 DR InterPro; IPR001227; Ac_transferase.
 DR InterPro; IPR003880; Peptide_attach.
 DR Pfam; PF00698; Acyl_transf_1.
 DR Pfam; PF0109; ketoacyl-synt_1.
 DR Pfam; PF02801; ketoacyl-synt_C; 1.
 DR Pfam; PF05507; Ac_DOMAIN; 1.
 DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
 DR PROSITE; PS00012; PHOSPHOPANTETHELINE; UNKNOWN_1.
 KW Phosphopantetheine; Transferase.
 SQ SEQUENCE 1832 AA; 193145 MW; C1EDB8F4473C2D2 CRC64;

DR Pfam; PF00550; PP-binding; 1.
 DR PROSITE; PS50075; ACP_DOMAIN; 1.
 DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
 DR PROSITE; PS00012; PHOSPHOPANTETHELINE; UNKNOWN_1.
 KW Phosphopantetheine; Transferase.
 SQ SEQUENCE 1832 AA; 193106 MW; E0DBA54B2B57DC91 CRC64;
 QY Query Match 38.1%; Score 54.5; DB 2; Length 1832;
 Best Local Similarity 54.2%; Pred. No. 39;
 Matches 13; Conservative 1; Mismatches 7; Indels 3; Gaps 1;
 QY 1 PWSP---SALRLQRPPEPPAANA 21
 DB 1123 PWPEVGLSLRLQRPSEGLMCHA 1146
 QY18Z8
 ID QY18Z8 PRELIMINARY; PRT; 1832 AA.
 AC QY18Z8;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)
 DE EPOC.
 GN EPOC.
 OS Polyangium cellulosum.
 OC Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
 OC Myxococcales; Sorangineae; Polyangiaceae; Polyangium.
 OX NCBI_TaxID=56;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SMP44;
 RX MEDLINE=20293058; PubMed=1081849;
 RA Julien B., Shah S., Ziermann R., Goldman R., Katz L., Khosia C.;
 RT "Isolation and characterization of the epothilone biosynthetic gene
 cluster from Sorangium cellulosum.";
 RL Gene 249:153-160(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SMP44;
 RX MEDLINE=20115953; PubMed=10649995;
 RA Tang L., Shah S., Chung L., Garney J., Katz L., Khosia C.,
 RT "Cloning and heterologous expression of the epothilone gene cluster.";
 RL Science 287:640-642(2000).
 DR EMBL; AF217189; AAF62882.1; -;
 DR InterPro; IPR001227; Ac_transferase.
 DR InterPro; IPR007943; Ketoacyl_synth.
 DR InterPro; IPR003880; Peptide_attach.
 DR Pfam; PF00698; Acyl_transf_1.
 DR Pfam; PF0109; ketoacyl-synt_1.
 DR Pfam; PF02801; ketoacyl-synt_C; 1.
 DR Pfam; PF05507; PP-binding; 1.
 DR PROSITE; PS50075; ACP_DOMAIN; 1.
 DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
 DR PROSITE; PS00012; PHOSPHOPANTETHELINE; UNKNOWN_1.
 KW Phosphopantetheine; Transferase.
 SQ SEQUENCE 1832 AA; 193145 MW; C1EDB8F4473C2D2 CRC64;
 QY Query Match 38.1%; Score 54.5; DB 2; Length 1832;
 Best Local Similarity 54.2%; Pred. No. 39;
 Matches 13; Conservative 1; Mismatches 7; Indels 3; Gaps 1;
 QY 1 PWSP---SALRLQRPPEPPAANA 21
 DB 1123 PWPEVGLSLRLQRPSEGLMCHA 1146
 QY18Z8
 ID QY18Z8 PRELIMINARY; PRT; 298 AA.
 AC QY18Z8;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, last sequence update)

01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE CBP protein.
 GN CBP OR BCDNA:GH12350 OR CG1435.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanalides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner K., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Adayani A., An H.-J., Andrews-Plamkoc C., Baldwin D.,
 RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertan B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Butris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris J.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibbegan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., Mcleod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner C., Ventler E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhou X., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Ventler J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CANTON S;
 RA Avedisov S.N.;
 RT Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G.,
 RA Adayani A., Arcaina T.T., Baxter E., Blazey R.G., Butenoff C.,
 RA Champe M., Chavez C., Chew M., Doyle C.M., Farlan D.E., Frise E.,
 RA Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M.,
 RA Houston K.A., Hummasti S.R., Kim E., Li F., Moshrefi M., Pacleb J.M.,
 RA Park S., Segueira A., Seth H., Snir E., Svirskas R.R., Weinburg T.,
 RA Celniker S.E.;
 RT "Full length Drosophila melanogaster cDNA sequence.";
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AEO03440; AAF46255.1; -
 DR EMBL: AP104405; AAC98512.1; -
 DR EMBL: AET145673; AAD38630.1; -
 DR HSSP: P04571; 2SCP.
 DR FlyBase: FBgn0026144; CBP.
 DR InterPro: IPR002048; EF-hand.

DR Pfam: PF00036; efhand. 3.
 DR SMART: SM00054; EFh. 2.
 DR PROSITE: PS00018; EF_HAND; UNKNOWN_2.
 SQ SEQUENCE 298 AA; 33983 MW; 1CA9717E8DC63E8 CRC64;
 Query Match 36.48; Score 52; ID 5; Length 298;
 Best Local Similarity 53.88; Pred. NO. 15;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 13 PEEPPAAHNR 25
 DB 36 PNTPTSHSDYHR 48
 RESULT 13
 ID Q8WMP8 PRELIMINARY; PRT: 2022 AA.
 AC Q8WMP8.
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-JUN-2002 (TReMBLrel. 20, Last sequence update)
 DE Voltage-gated sodium channel alpha subunit.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Kuminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HEART;
 RA Denne H., Meyersen M., Lis J.L., Haltiner R., Scholtysik G.;
 RT "Molecular cloning of a putative bovine heart voltage gated sodium
 channel isoform.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ251721; CAC80974.1; -
 DR InterPro: IPR001682; Ca/Na_Pore.
 DR InterPro: IPR002111; Cat_channel_TripL.
 DR InterPro: IPR000048; IQ_region.
 DR InterPro: IPR000636; M_channel_nlg.
 DR Pfam: PF00520; Ion_channel.
 DR Pfam: PF00612; Ion_trans. 4.
 DR PRINTS: PR00170; NACHANNEL.
 DR Tonic channel.
 SQ SEQUENCE 2022 AA; 227892 MW; 5B7C9E08H1958779 CRC64;
 Query Match 36.48; Score 52; ID 6; Length 2022;
 Best Local Similarity 71.48; Pred. NO. 97;
 Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 9 LIDRPPPPAAHNR 22
 DB 989 LIDRPPCKPAALAS 1002
 RESULT 14
 ID Q9LVX4 PRELIMINARY; PRT: 128 AA.
 AC Q9LVX4.
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Gb1AAB60912.1.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eustids II; Brassicales; Brassicaceae; Arabidopsis.
 NC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asanizu E., Tabata S.;
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.

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RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20277480; PubMed=10319329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones."
RL DNA Res. 7:131-135(2000).
DR EMBL: AB018114; BAB02689.1; -.
DR InterPro: IPR004883; DUF260.
DR Pfam: PF03195; DUF260; 1.
SQ SEQUENCE 128 AA; 1418 MW; A278F8525A29DABF CRC64;

Query Match
Best Local Similarity 36.0%; Score 51.5; DB 10; Length 128;
Matches 14; Conservative 3; Mismatches 6; Indels 13; Gaps 2;

QY 3 SP-SALRLIQR-----PPEPAHANCHR 25
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Db 7 SPCACKFLRKCTSDCVFAPYPPEPTKFAVNR 42

RESULT 15
Q8W1D6 PRELIMINARY; PRT; 159 AA.
AC Q8W1D6;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Ldb domain 25.
GN LBD25.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=9702;
RN 111
RP SEQUENCE FROM N.A.
RA Shuai B., Reynaga-Pena G., Springer P.S.;
RT "The LATERAL ORGAN BOUNDARIES Gene Defines a Novel, Plant-Specific
RT Gene Family."
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF447892; AAL38017.1; -.
DR InterPro: IPR004883; DUF260.
DR Pfam: PF03195; DUF260; 1.
SQ SEQUENCE 159 AA; 17749 MW; 6B9F9D5FA7818BBF CRC64;

Query Match
Best Local Similarity 36.0%; Score 51.5; DB 10; Length 159;
Matches 14; Conservative 3; Mismatches 6; Indels 13; Gaps 2;

QY 3 SP-SALRLIQR-----PPEPAHANCHR 25
   || : | : ||
Db 38 SPCACKFLRKCTSDCVFAPYPPEPTKFAVNR 73

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Search completed: March 13, 2003, 12:37:19
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